

Fig. 1A

1 GCTACCTCCA ACTGCTGAGG ACCGGTTGC CTAAGAGGAG CCGGCAAAAG
 51 CGCCTACGTG GAGTCCAGAG GAGCGGAAGT AGTCAGATT GACTGAGAGC
 101 CGTAAAGCGC GGCTGGCTCT CGTTTCCGG ATAACGACTA CAGCTCCGAC
 151 TGTCAAGTGC GGCCCTCCCT GTGTGAGGGG ATCTGCCGGA CCCCTGCAA
 201 TTCAATTCTTCC TCCCCATTCC GGGCCCTTCC CTATCGTCGC CCCCTTCACC
 251 TTGGATCATG TTCAAGAAAT TTGATGAAAA AGAAAATGTG TCCAACGTCA
 301 TCCAGTTGAA AACTTCAGTT ATAAGGGTA TTAAGAATCA ATTGATAGAG
 351 CAATTCCAG GTATTGAACC ATGGCTTAAT CAAATCATGC CTAAGAAAGA
 401 TCCTGTCAAA ATAGTCCGAT GCCATGAACA TATAGAAATC CTTACAGTAA
 451 ATGGAGAATT ACTCTTTT AGACAAAGAG AAGGGCCTT TTATCCAACC
 501 CTAAGATTAC TTACAAATA TCCTTTTATC CTGCCACACC AGCAGGTGAA
 551 TAAAGGAGCC ATCAAATTG TACTCAGTGG AGCAAATATC ATGTGTCCCA
 601 GGCTTAACCT CTCCCTGGAGC TAAGCTTAC CCTGGCTGCAG TAGATAACCAT
 651 TGTTGCTATC ATGGCAGAAG GAAAACAGCA TGCTCTATGT GTTGGAGTCA
 701 TGAAGATGTC TGCAGAAGAC ATGAGAAAG TCAACAAAGG AATTGGCATT
 751 GAAAATATCC ATTATTAAA TGATGGCTG TGGCATATGA AGACATATAA
 801 ATGAGCCCTCA GAAGGAATGC ACTTGGCTA AATATGGATA TTGTGCTGTA
 851 TCTGTGTTG TGTCTGTG TGACAGCATG AAGATAATGC CTGTGGTTAT
 901 GCTGAATAAA TTCACCAAGAT GCTAAAGAA AAAAAGAA AAAA

Fig. 1B

1 M F K K F D E K E N V S N C I Q L K T S V I K G I K N
 28 Q L I E Q F P G I E P W L N Q I M P K K D P V K I V R
 55 C H E H I E I L T V N G E L L F F R Q R E G P F Y P T
 82 L R L L H K Y P F I L P H Q Q V D K G A I K F V L S G
 109 A N I M C P R L N F S W S

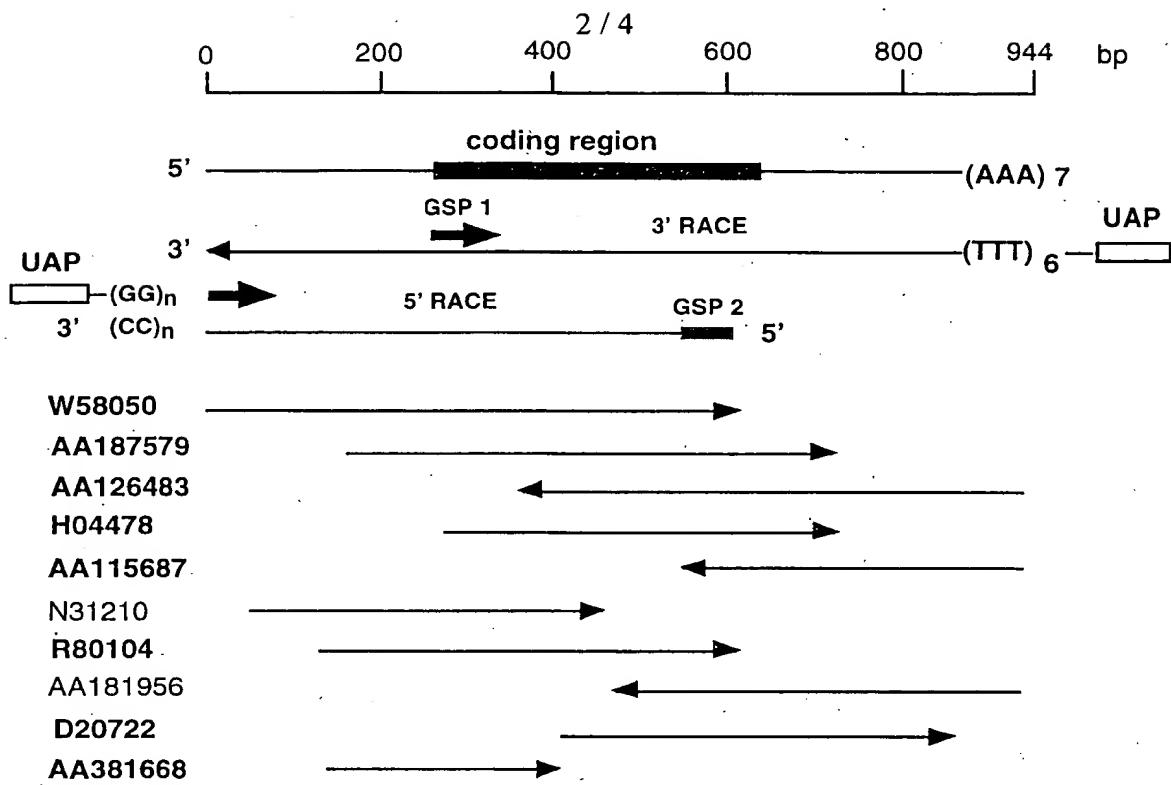


Fig. 2

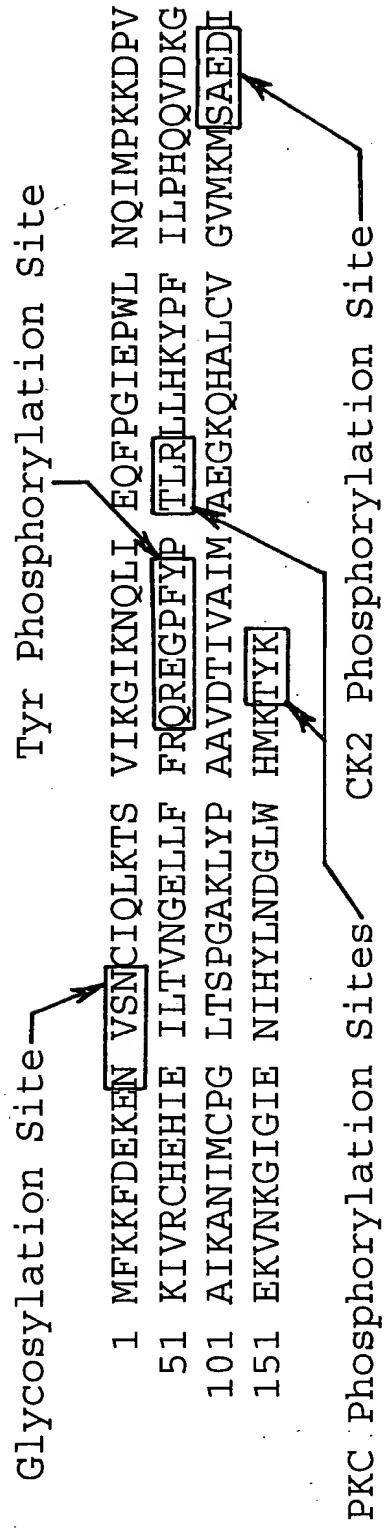


Fig. 3

MCF-1 8 KENVSNCIQLKTSVIKGIKNQLIEQFPGIEPWL NQIMPKKDPV K 51
 Cyclin H 239 KEN . RTCLSQLLDIMKSMRN . LVKKYE . PPRSEEVAVLKQ . . K277

MCF-1 52 IVRCHEHIEILTVN 65
 Cyclin H 278 LERCHS . AE . LALN 288

Fig. 4

Fig. 5A

1 GCTACCTCCA ACTGCTGAGG AACCGGTGAC CTAAGAGGAG CCGGAAAG
 51 CGCCTACGTG GAGTCCAGAG GAGCGGAAGT AGTCAGATT GACTGAGAGC
 101 CGTAAAGCGC GGCTGGCTCT CGTTTCCGG ATAACGACTA CAGCTCCGAC
 151 TGTCAAGTGC GGCCTCCCTC GTGTGAGGGG ATCTGCCGG CCCCTGCAA
 201 TTCAATTCTC TCCCCATTCC GGGCCCTTCC CTATGTCGC CCCCTCACCC
 251 TTGGATC**A**TG TTCAAGAAAT TTGATGAAAA AGAAAATGTTG TCCAAGTGC
 301 TCCAGTTGAA AACTTCAGTT ATAAGGGTA TAAGAATCA ATTGATAGAG
 351 CAATTCCAG GTATTGAACC ATGGCTTAAT CAAATCATGC CTAAGAAAGA
 401 TCCTGTCAA ATAGTCCGAT GCCATGAACCA TATAGAAATC CTTACAGTAA
 451 ATGGAGAATT ACTCTTTT AGACAAAGAG AAGGGCCTT TTATCCAACC
 501 CTAAGATTAC TTCAACAAATA TCCTTTTATC CTGCCACACC AGCAGGTTGA
 551 TAAAGGAGCC ATCAAATTG TACTCAGTGG AGCAAATATC ATGTGTCCAG
 601 GCTTAACCTC TCCTGGAGCT AAGCTTTACC CTGCTGCAGT AGATACCATT
 651 GTTGCTATCA TGGCAGAAGG AAAACAGCAT GCTCTATGTG TTGGAGTCAT
 701 GAAGATGTCT GCAGAAGACA TTGAGAAAGT CAACAAAGGA ATTGGCATG
 751 AAAATATCCA TTATTTAAAT GATGGGCTGT GGCAATATGAA GACATATAAA
 801 **TGAGCCTCAG** AAGGAATGCA CTGGGCTAA ATATGGATAT TGTGCTGTAT
 851 CTGTGTTGT GTCTGTGT GACAGCATGA AGATAATGCC TGTGGTTATG
 901 CTGAATAAAAT TCACCAAGATG CTAAGAAAAA AAAAAGAAA AAA

Fig. 5B

1 M F K K F D E K E N V S N C I Q L K T S V I K G I K N
 28 Q L I E Q F P G I E P W L N Q I M P K K D P V K I V R
 55 C H E H I E I L T V N G E L L F F R Q R E G P F Y P T
 82 L R L L H K Y P F I L P H Q Q V D K G A I K F V L S G
 109 A N I M C P G L T S P G A K L Y P A A V D T I V A I M
 136 A E G K Q H A L C V G V M K M S A E D I E K V N K G I
 163 G I E N I H Y L N D G L W H M K T Y K